ETS1 suppresses Tumorigenesis of Human Breast Cancer via Trans-Activation of Canonical Tumor Suppressor Genes

Gi-Cheon Kim^{1,2}, *Choong-Gu Lee*³, *Ravi Verma*⁴, *Dipayan Rudra*⁴, *Taemook Kim*⁵, *Keunsoo Kang*⁶, *Jong Hee Nam*⁷, *Young Kim*⁸, *Sin-Hyeog Im*^{4,9} and *Ho-Keun Kwon*^{1,2,10*}

¹ Department of Microbiology and Immunology, Yonsei University College of Medicine, Seoul, South Korea, ² Institute for Immunology and Immunological Diseases, Yonsei University College of Medicine, Seoul, South Korea, ³ Natural Product Informatics Research Center, Korea Institute of Science and Technology (KIST), Gangneung Institute of Natural Products, Gangneung, South Korea, ⁴ Academy of Immunology and Microbiology (AIM), Institute for Basic Science (IBS), Pohang, 37673, Republic of Korea, ⁵ Department of Biological Sciences, Korea Advanced Institute of Science and Technology, Daejeon, South Korea, ⁶ Department of Microbiology, College of Natural Sciences, Dankook University, Cheonan, South Korea, ⁷ Chonnam National University Medical School, Gwangju, South Korea, ⁸ Department of Oral Pathology, School of Dentistry, Chonnam National University, Gwangju, South Korea, ⁹ Division of Integrative Biosciences and Biotechnology, Department of Life Sciences, Pohang University of Science and Technology, Pohang, South Korea, ¹⁰ Brain Korea 21 PLUS Project for Medical Sciences, Yonsei University College of Medicine, Seoul, South Korea

*Correspondence: HK@yuhs.ac

*Address correspondence to: Dr. Ho-Keun Kwon, Department of Microbiology and Immunology, Yonsei University College of Medicine; Brain Korea 21 PLUS Project for Medical Sciences, Institute for Immunology and Immunological Diseases. 50-1 Yonse-ro, Seodaemin-gu, Seoul, South Korea, 03722; Tel: 82-2-2228-1818; Email: HK@yuhs.ac

Supplementary Information

Supplementary Figure 1. Comparison of *ETS1* expression between normal and tumor patient specimens in publically available dataset (Curtis).

Supplementary Figure 2. Comparison of *ETS1* expression between normal and tumor patient specimens in diverse cancer types.

Supplementary Figure 3. DNA methylation status on *ETS1* promoter (locus #1) in diverse normal and tumor specimens.

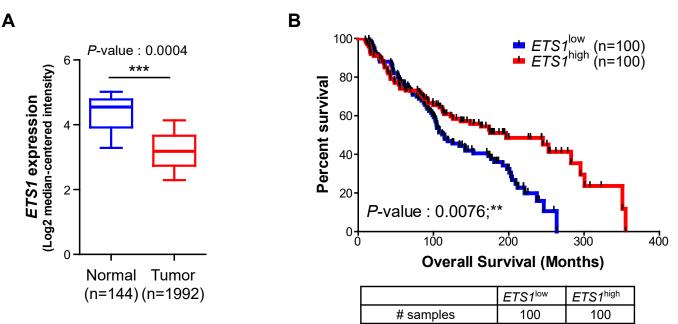
Supplementary Figure 4. ETS1 inhibits the proliferation and growth of MCF-7 breast cancer cells *in vitro* as well as *in vivo*.

Supplementary Figure 5. Bioinformatic analysis of promoter regions of representative ETS1 target genes **Supplementary Figure 6.** Full Immuno-blots of the experiments

Supplementary Table 1. Primer sequences used for qRT-PCR
Supplementary Table 2. Primer sequences used for ChIP-PCR.
Supplementary Table 3. Correlation between methylation value of CpG site and *ETS1* expression in normal and tumor specimens.
Supplementary Table 4. Differential expressed genes (DEGs) in RNA-seq
Supplementary Table 5. Gene Ontology of DEG
Supplementary Table 6. List of Tumor suppressor genes (TSGs)

Supplementary Table 7. Overlap DEGs with TSGs

Supplementary Figure 1.



		-
# samples	100	100
# censored subjects	30	47
# deaths/events	70	53
Median survival	114.533	196.567

Triple negative	Non-triple negative	Total
299	1605	1904
161	942	1103
25	67	92
14	39	53
56.0	58.2	57.6
8.4	4.2	4.8
	negative 299 161 25 14 56.0	negative negative 299 1605 161 942 25 67 14 39 56.0 58.2

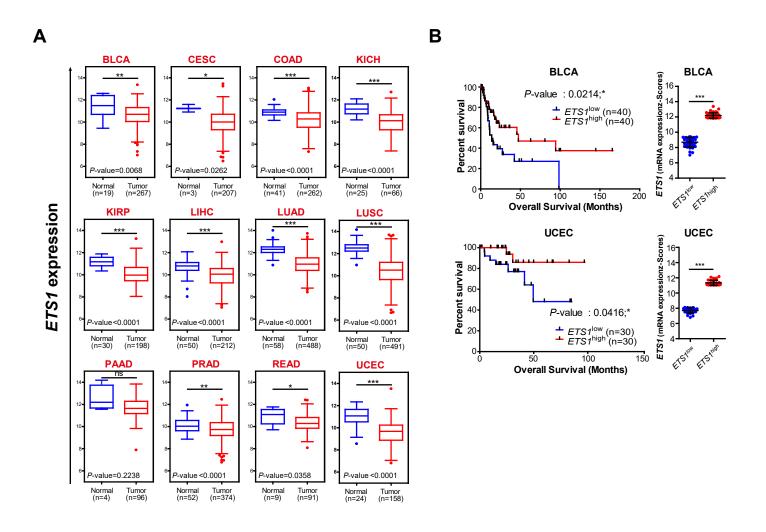
D

С

	Triple negative	Non-triple negative	Total
Total number	116	803	919
Death number	18	78	96
Mutation number	11	68	79
Death in Mutation	1	9	10
Mutation & Death ratio (%)	9.1	13.2	12.7
Mutation ratio (%)	9.5	8.5	8.6

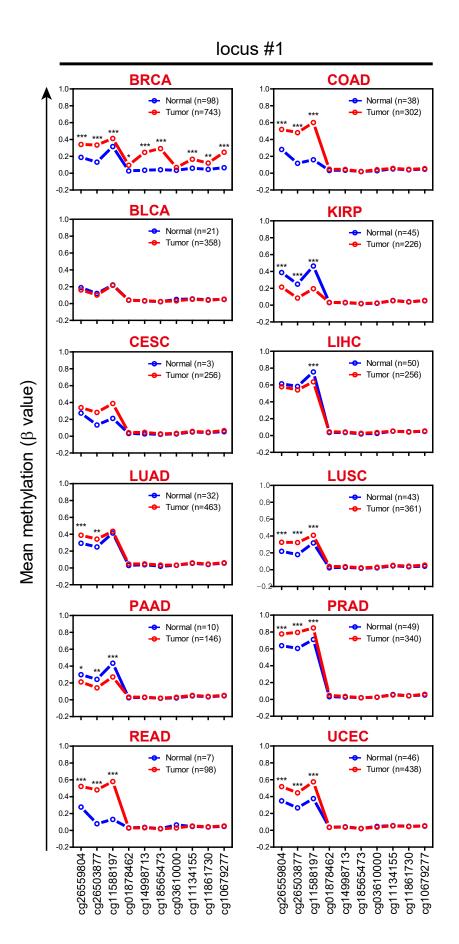
Supplementary Figure 1. Comparison of *ETS1* expression between normal and tumor patient specimens in publically available dataset (Curtis). (**A**) Box plot of *ETS1* gene expression between normal and breast cancer tissues in publically available Curtis data set; normal (n=144) and tumor (n=1992). ***P<0.001 (Unpaired t test). (**B**) Correlation between *ETS1* expression and survival rate. A total of 1992 samples were divided into *ETS1*^{high} group (n = 100) and *ETS1*^{low} (n = 100) according to *ETS1* expression levels (*ETS1*^{low} or *ETS1*^{high} selection criteria are each less than the lower or higher 10% of the total patient). Overall survival analysis based on *ETS1* levels in BRCA patient. The blue or red lines indicate patients with *ETS1*^{low} (n=100) or *ETS1*^{high} expression (n=100), respectively. *P*-value was calculated with the Log-rank test (*P*-value = 0.0076;**). (**C-D**) Correlation between genetic alteration and survival rate of *ETS1* according to breast cancer subtype in (**C**) Curtis data set and (**D**) TCGA data set.

Supplementary Figure 2.



Supplementary Figure 2. Comparison of ETS1 expression between normal and tumor patient specimens in diverse cancer types. (A) Tumor types that show a reduced ETS1 expression. BLCA: Bladder Urothelial Carcinoma; CESC: Cervical squamous cell carcinoma and endocervical adenocarcinoma; COAD: colon adenocarcinoma; KICH: Kidney Chromophobe; KIRP: Kidney renal papillary cell carcinoma; LIHC: Liver hepatocellular carcinoma; LUAD: Lung adenocarcinoma; LUSC: PAAD: Pancreatic Lung squamous carcinoma; adenocarcinoma; PRAD: Prostate cell adenocarcinoma; READ: Rectum adenocarcinoma; UCEC: Uterine corpus endometrial carcinoma. *P<0.05, **P<0.01, ***P<0.001 (Unpaired t test). (B) Overall survival analysis based on ETS1 levels in BLCA, UCEC. The blue or red lines indicate patients with ETS1^{low} or ETS1^{high} expression, respectively. P-value was calculated with the Log-rank test (*P<0.05) and ***P<0.001 (Unpaired t test).

Supplementary Figure 3.

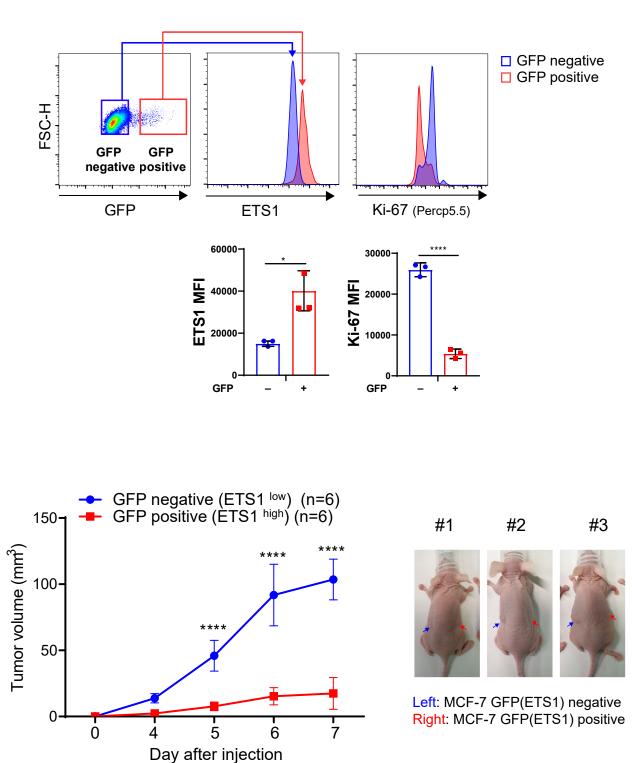


Supplementary Figure 3. DNA methylation status on ETS1 promoter (locus #1) in diverse normal and tumor specimens. Analysis of mean methylation β -value on 10 CpG sites of *ETS1* locus #1 between normal (n=98) and BRCA patient (n=743) specimens by TCGA Wanderer tool. The blue or red line represents normal or BRCA specimen, respectively. *P<0.05, **P<0.01, ***P<0.001 (two-way ANOVA with Bonferroni test).

Supplementary Figure 4.

Α

В



Supplementary Figure 4. ETS1 inhibits the proliferation and growth of MCF-7 breast cancer cells *in vitro* as well as *in vivo*. (**A**) MCF-7 cells (ER+, PR+ and HER2-; no ETS1 expression) were transfected with Human cDNA ETS1 GFP vector, and transfected cells were sorted according to GFP -expression. Representative data from three independent experiments. Flow cytometry analysis for ETS1 protein levels and cell proliferation (Ki -67) in GFP negative and positive. *P<0.05, **P<0.01, ***P<0.001 ****P<0.001 (Unpaired t test). (**B**) Tumor growth curves in nude mice after injection of GFP negative (left) and positive (right) MCF-7 cells. Tumor volumes were measured. Images of representative tumor-bearing mice. Blue arrow: MCF-7 GFP(ETS1) negative; Red arrow: MCF-7 GFP(ETS1) positive. *P<0.05, **P<0.01, ***P<0.001 ****P<0.001 (two-way ANOVA with Bonferroni test). Data is representative of three independent experiments.

ADAMTS9

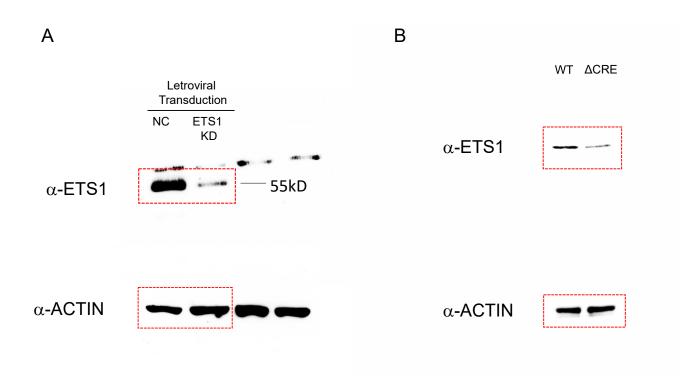
А

A	ADAMI 59	Rea: EIST binding site
	> hg19 chr3:64673012-64674054 1243bps TAAAATAAAACATGACGCTATCTGGTGCCCCCAATTACTAAGTTACTTTAGTTTGCGGCGTGGG AGTGGGGATGGGGATATATCTGGCAACAGCAAGGAAGGGGGGGG	Green: ChIP primer
В	NOTCH1 > hg19 chr9:139440638-139440858 421bps CCCGCCCCGCCCGGCCCCGCCCGCGCGCGCGCGCGCGC	
С	TXNIP > hg19 chr1:145438265-145438510 446bps GGCTAGGTTTTAGGGTCAGTGGGATCCTCCTTCCACTGGACCCGGGAGAAGACGCTCAACAG ccccctccttccctccttccttccttccttcctcccccc	
D	STAT5A > hg19 chr17:40437576-40437785 410bps ATTTGGGGGTGAAGAGCAGTTAGGGGCAAGGAGGCCAGCCTCGGACCGCAGCTCAGTCAG	

Red: ETS1 binding sites

Supplementary Figure 5. Bioinformatic analysis of promoter regions of representative ETS1 target genes (A) *ADAMTS9*, (B) *NOTCH1*, (C) *TXNIP* and (D) *STAT5A* promoter sequences were analyzed by ECR browser

Supplementary Figure 6.



Supplementary Figure 6. Full Immuno-blots of the experiments shown in (**A**) Figure 3A (**B**) Figure 3C. Uncropped images are labeled as in the main text and red dot square indicate protein bands of interest.